REMARKS

Entry of all amendments before examination of the application is respectfully requested. Claims 1 through 57 are pending in this application. Claims 1, 2, 11, 12, 21, 22, 31, 32 and 33 have been amended. These claims were amended to reference SEQ ID NOS to a sequence listing being filed herewith. The sequences referenced are found in Figures 1 through 6. The Claims 34 through 57 were added in this amendment. Support for these claims is found on page 30, lines 1 through 23. Please enter the Sequence Listing containing SEQ ID NO: 1 through SEQ ID NO: 15. No new matter has been added by these amendments.

In light of the above amendment and remarks, Applicant asserts that the claims are now in condition for allowance. Accordingly, Applicant respectfully requests that the Examiner issue a Letters Patent on the present application.

Applicant authorizes the charging of any required fees to Account No. 06-2375/09807797, from which the undersigned is authorized to draw. If there are any questions regarding this Amendment and Response or the application in general, please do not hesitate to contact the undersigned.

Respectfully submitted,

Date: 04-27-01

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

The paragraph beginning at page 4, line 2 has been amended as follows:

--FIG. 1 shows the 1276 base pair cDNA sequence of gene O1-180 (SEQ ID NO: 1).--

The paragraph beginning at page 4, line 3, has been amended as follows:

--FIG. 2 shows the 361 amino acid sequence that is coded for by gene O1-180 (SEQ ID NO: 2).--

The paragraph beginning at page 4, line 4, has been amended as follows:

--FIG. 3 shows the 1817 base pair cDNA sequence of gene O1-184 (SEQ ID NO: 3).--

The paragraph beginning at page 4, line 5, has been amended as follows:

--FIG. 4 shows the 426 amino acid sequence that is coded for by gene O1-184 (SEQ ID NO: 4).--

The paragraph beginning at page 4, line 6, has been amended as follows:

--FIG. 5 shows the 1019 base pair cDNA sequence of gene O1-236 (SEQ ID NO: 5).--

The paragraph beginning at page 4, line 7, has been amended as follows:

--FIG. 6 shows the 207 amino acid sequence that is coded for by gene O1-236 (SEQ ID NO: 6).--

The paragraph beginning at page 4, line 30, has been amended as follows:

--FIG. 10. Npm2 cDNA representation. Schematic representation of the mouse Npm2 cDNA sequence (984 bp) and two of the clones isolated from the mouse ovary CDNA libraries. The original 01-236 probe (749 bp) is shown at the top and encompasses the entire Npm2 open reading frame. The open reading frame (solid box) is 621 bp and the 5' UTR and 3' UTR

sequences (thin lines) are 155 bp and 205 bp, respectively. The polyA sequences are not depicted. Clone 236-1 was isolated from the wild-type ovary cDNA library and clone 236-3 was isolated from the GDF-9-deficient ovary cDNA library. Clone 236-3 (984 bp excluding polyA sequence) is 4 bp longer at the 5' end and 1 bp longer at the 3' end than clone 236-1 (979 bp excluding polyA sequences). Codon 36 of the open reading frame of both cDNAs is GGC (Glycine; Figure 11) whereas the same codon of the 129SvEv gene is TGC (Cysteine; [Figure 13] Figures 13A and 13B (SEQ ID NO: 7 through SEQ ID NO: 14)).--

The paragraph beginning at page 5, line 28, has been amended as follows:

--FIGS. 13A and 13B. Mouse Npm2 gene (SEQ ID NO: 7 through SEQ ID NO: 14) and amino acid sequences. Uppercase letters represent sequence identity with the Npm2 cDNA sequences; non-transcribed 5' and 3' sequences and intron sequences are shown in lowercase. The predicted transcription initiation codon, the termination codon, and the polyadenylation signal sequence are all underlined. Numbers along the left side represent the amino acids. The underlined and [bloded] bolded "T" in codon 36, the bolded "c" for amino acid 26, and the underlined and bolded "C: in the 3' UTR sequence indicate differences between the cDNA and gene sequences. Arrows indicate where the O1-236 fragment initiates and ends in the cDNA sequence.--

The paragraph beginning at page 10, line 15, has been amended as follows:

--Fragments of proteins are seen to include any peptide that contains 6 contiguous amino acids or more that are identical to 6 contiguous amino acids of either of the sequences shown in Figures 2 (SEQ ID NO: 2), 4 (SEQ ID NO: 4), 6 (SEQ ID NO: 6), 11 and 14. Fragments that contain 7, 8, 9, 10, 11, 12, 13, 14 and 15 or more contiguous amino acids or more that are identical to a corresponding number of amino acids of any of the sequences shown in Figures 2 (SEQ ID NO: 2), 4 (SEQ ID NO: 4), 6 (SEQ ID NO: 6), 11 and 14 are also contemplated. Fragments may be used to generate antibodies. Particularly useful fragments will be those that make up domains of O1-180, O1-184 or O1-236. Domains are defined as portions of the proteins having a discrete tertiary structure and that is maintained in the absence of the remainder of the protein. Such structures can be found by techniques known to those skilled in the art. The protein is partially